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Figure 1: Nucleotide and amino acid sequences (SEQ ID Nos: 1 and 2) of the ATP/ADP translocase from *Chlamydia pneumonia*

| | | | | | | |
|---|------------|------------|-------------|----------|---------|----|
| gaaataaaaa | actatcagaa | tagaaaataa | aagtattttca | gagggtaa | atg aca | 56 |
| | | | | | Met Thr | |
| | | | | | 1 | |
| aaa acc gaa gaa aaa cct ttt gga aaa ttg cgc tct ttc ttg tgg ccg | 104 | | | | | |
| Lys Thr Glu Glu Lys Pro Phe Gly Lys Leu Arg Ser Phe Leu Trp Pro | | | | | | |
| 5 10 15 | | | | | | |
| ata cat act cac gag cta aag aaa gtt ctg cca atg ttc cta atg ttc | 152 | | | | | |
| Ile His Thr His Glu Leu Lys Lys Val Leu Pro Met Phe Leu Met Phe | | | | | | |
| 20 25 30 | | | | | | |
| ttc tgt att aca ttt aac tat acg gtg tta cgc gat aca aaa gac act | 200 | | | | | |
| Phe Cys Ile Thr Phe Asn Tyr Thr Val Leu Arg Asp Thr Lys Asp Thr | | | | | | |
| 35 40 45 50 | | | | | | |
| ctt att gtg gga gct cct ggt tct ggt gca gag gca ata cct ttc atc | 248 | | | | | |
| Leu Ile Val Gly Ala Pro Gly Ser Gly Ala Glu Ala Ile Pro Phe Ile | | | | | | |
| 55 60 65 | | | | | | |
| aag ttt tgg ctt gtt gtc ccc tgt gct att atc ttt atg ctt att tat | 296 | | | | | |
| Lys Phe Trp Leu Val Val Pro Cys Ala Ile Ile Phe Met Leu Ile Tyr | | | | | | |
| 70 75 80 | | | | | | |
| gca aag cta agt aat att tta agt aag cag gcc tta ttt tat gca gtg | 344 | | | | | |
| Ala Lys Leu Ser Asn Ile Leu Ser Lys Gln Ala Leu Phe Tyr Ala Val | | | | | | |
| 85 90 95 | | | | | | |
| gga acg ccc ttt tta att ttc ttt gcc ctg ttc ccg act gta att tat | 392 | | | | | |
| Gly Thr Pro Phe Leu Ile Phe Phe Ala Leu Phe Pro Thr Val Ile Tyr | | | | | | |
| 100 105 110 | | | | | | |
| ccg cta cgc gat gtt tta cat cct aca gaa ttt gct gac cgt tta cag | 440 | | | | | |
| Pro Leu Arg Asp Val Leu His Pro Thr Glu Phe Ala Asp Arg Leu Gln | | | | | | |
| 115 120 125 130 | | | | | | |
| gcc atc cta cct cca gga ttg cta gga ctc gtt gcc atc tta aga aac | 488 | | | | | |
| Ala Ile Leu Pro Pro Gly Leu Leu Gly Leu Val Ala Ile Leu Arg Asn | | | | | | |
| 135 140 145 | | | | | | |
| tgg aca ttt gct gca ttt tat gta ctt gct gaa cta tgg gga agc gtc | 536 | | | | | |
| Trp Thr Phe Ala Ala Phe Tyr Val Leu Ala Glu Leu Trp Gly Ser Val | | | | | | |
| 150 155 160 | | | | | | |
| atg cta tct cta atg ttc ttg gga ttt gct aat gaa att aca aaa atc | 584 | | | | | |
| Met Leu Ser Leu Met Phe Trp Gly Phe Ala Asn Glu Ile Thr Lys Ile | | | | | | |
| 165 170 175 | | | | | | |
| cac gaa gca aag cgt ttc tac gct ctt ttc ggt atc gga gct aat att | 632 | | | | | |
| His Glu Ala Lys Arg Phe Tyr Ala Leu Phe Gly Ile Gly Ala Asn Ile | | | | | | |
| 180 185 190 | | | | | | |

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Figure 1 (continued)

| | |
|---|------|
| tct tta cta gct tct ggt cgt gca att gtt tgg gct tca aag ttg aga | 680 |
| Ser Leu Leu Ala Ser Gly Arg Ala Ile Val Trp Ala Ser Lys Leu Arg | |
| 195 200 205 210 | |
| gct tcc gtt tct gaa ggt gta gat cct tgg gga att tct tta cgt ctt | 728 |
| Ala Ser Val Ser Glu Gly Val Asp Pro Trp Gly Ile Ser Leu Arg Leu | |
| 215 220 225 | |
| ttg atg gct atg act att gta tct gga ctt gtt ctt atg gcc agt tac | 776 |
| Leu Met Ala Met Thr Ile Val Ser Gly Leu Val Leu Met Ala Ser Tyr | |
| 230 235 240 | |
| tgg tgg atc aat aag aac gta ttg acc gat cct cgc ttc tat aat cca | 824 |
| Trp Trp Ile Asn Lys Asn Val Leu Thr Asp Pro Arg Phe Tyr Asn Pro | |
| 245 250 255 | |
| gaa gaa atg caa aag ggg aaa aaa ggt gct aaa cct aaa atg aat atg | 872 |
| Glu Glu Met Gln Lys Gly Lys Lys Gly Ala Lys Pro Lys Met Asn Met | |
| 260 265 270 | |
| aaa gat agc ttc ctc tat ctt gat aga tct cct tat att ctt tta tta | 920 |
| Lys Asp Ser Phe Leu Tyr Leu Asp Arg Ser Pro Tyr Ile Leu Leu Leu | |
| 275 280 285 290 | |
| act ctc ttg gtt att gcc tat ggt att tgc att aac tta atc gaa gtg | 968 |
| Thr Leu Leu Val Ile Ala Tyr Gly Ile Cys Ile Asn Leu Ile Glu Val | |
| 295 300 305 | |
| act tgg aaa agt cag ctg aaa ctg caa tat cct aat atg aat gac tat | 1016 |
| Thr Trp Lys Ser Gln Leu Lys Leu Gln Tyr Pro Asn Met Asn Asp Tyr | |
| 310 315 320 | |
| agt gag ttc atg ggg aac ttc tcc ttc tgg act ggc gta gta tcc gta | 1064 |
| Ser Glu Phe Met Gly Asn Phe Ser Phe Trp Thr Gly Val Val Ser Val | |
| 325 330 335 | |
| ctt atc atg cta ttt gtt ggt ggt aac gtc att cgt aaa ttt gga tgg | 1112 |
| Leu Ile Met Leu Phe Val Gly Gly Asn Val Ile Arg Lys Phe Gly Trp | |
| 340 345 350 | |
| tta act gga gcc cta gtc act cct gtc atg gtt ctc cta aca ggt atc | 1160 |
| Leu Thr Gly Ala Leu Val Thr Pro Val Met Val Leu Leu Thr Gly Ile | |
| 355 360 365 370 | |
| gtt ttc ttc gct ctt gtt atc ttt aga aac caa gct tct ggg ctg gtc | 1208 |
| Val Phe Phe Ala Leu Val Ile Phe Arg Asn Gln Ala Ser Gly Leu Val | |
| 375 380 385 | |
| gct atg ttc ggt aca act cct ctc atg cta gct gtg gtt gtc gga gct | 1256 |
| Ala Met Phe Gly Thr Thr Pro Leu Met Leu Ala Val Val Val Gly Ala | |
| 390 395 400 | |
| ata cag aat att ctt tcg aaa tcc aca aaa tac gct ctc ttt gac tca | 1304 |
| Ile Gln Asn Ile Leu Ser Lys Ser Thr Lys Tyr Ala Leu Phe Asp Ser | |
| 405 410 415 | |

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Figure 1 (continued)

| | | | | | | | | | | | | | | | | |
|-----|-------|-------|--------|------|-------|-------|--------|------|-----|-----|-----|-----|-----|-----|-----|------|
| act | aaa | gaa | atg | gcc | tat | atc | cct | ctt | gac | caa | gag | caa | aaa | gtc | aaa | 1352 |
| Thr | Lys | Glu | Met | Ala | Tyr | Ile | Pro | Leu | Asp | Gln | Glu | Gln | Lys | Val | Lys | |
| | 420 | | | | | 425 | | | | | 430 | | | | | |
| ggt | aag | gct | gct | att | gat | gta | gtt | gcc | gcc | cgc | ttc | gga | aaa | tca | gga | 1400 |
| Gly | Lys | Ala | Ala | Ile | Asp | Val | Val | Ala | Ala | Arg | Phe | Gly | Lys | Ser | Gly | |
| | 435 | | | | 440 | | | | | 445 | | | | | 450 | |
| gga | gct | tta | atc | caa | caa | ggt | ttg | ctc | gtt | atc | tgt | gga | agt | att | gga | 1448 |
| Gly | Ala | Leu | Ile | Gln | Gln | Gly | Leu | Leu | Val | Ile | Cys | Gly | Ser | Ile | Gly | |
| | | | | 455 | | | | | 460 | | | | | 465 | | |
| gct | atg | acc | cct | tat | ctt | gca | gtg | att | ctt | ctt | ttc | atc | att | gct | att | 1496 |
| Ala | Met | Thr | Pro | Tyr | Leu | Ala | Val | Ile | Leu | Leu | Phe | Ile | Ile | Ala | Ile | |
| | | | 470 | | | | | 475 | | | | | 480 | | | |
| tgg | ttg | gtt | tct | gca | act | aag | tta | aac | aaa | cta | ttc | tta | gcg | cag | tct | 1544 |
| Trp | Leu | Val | Ser | Ala | Thr | Lys | Leu | Asn | Lys | Leu | Phe | Leu | Ala | Gln | Ser | |
| | 485 | | | | | | 490 | | | | | 495 | | | | |
| gct | ctt | aaa | gaa | caa | gaa | gtg | gct | caa | gaa | gat | tca | gct | cct | gct | tct | 1592 |
| Ala | Leu | Lys | Glu | Gln | Glu | Val | Ala | Gln | Glu | Asp | Ser | Ala | Pro | Ala | Ser | |
| | 500 | | | | | 505 | | | | 510 | | | | | | |
| tca | tagag | ttgct | tctctt | actc | ttgtt | gatcc | ctacct | gctt | tt | | | | | | | 1637 |
| Ser | | | | | | | | | | | | | | | | |
| 515 | | | | | | | | | | | | | | | | |

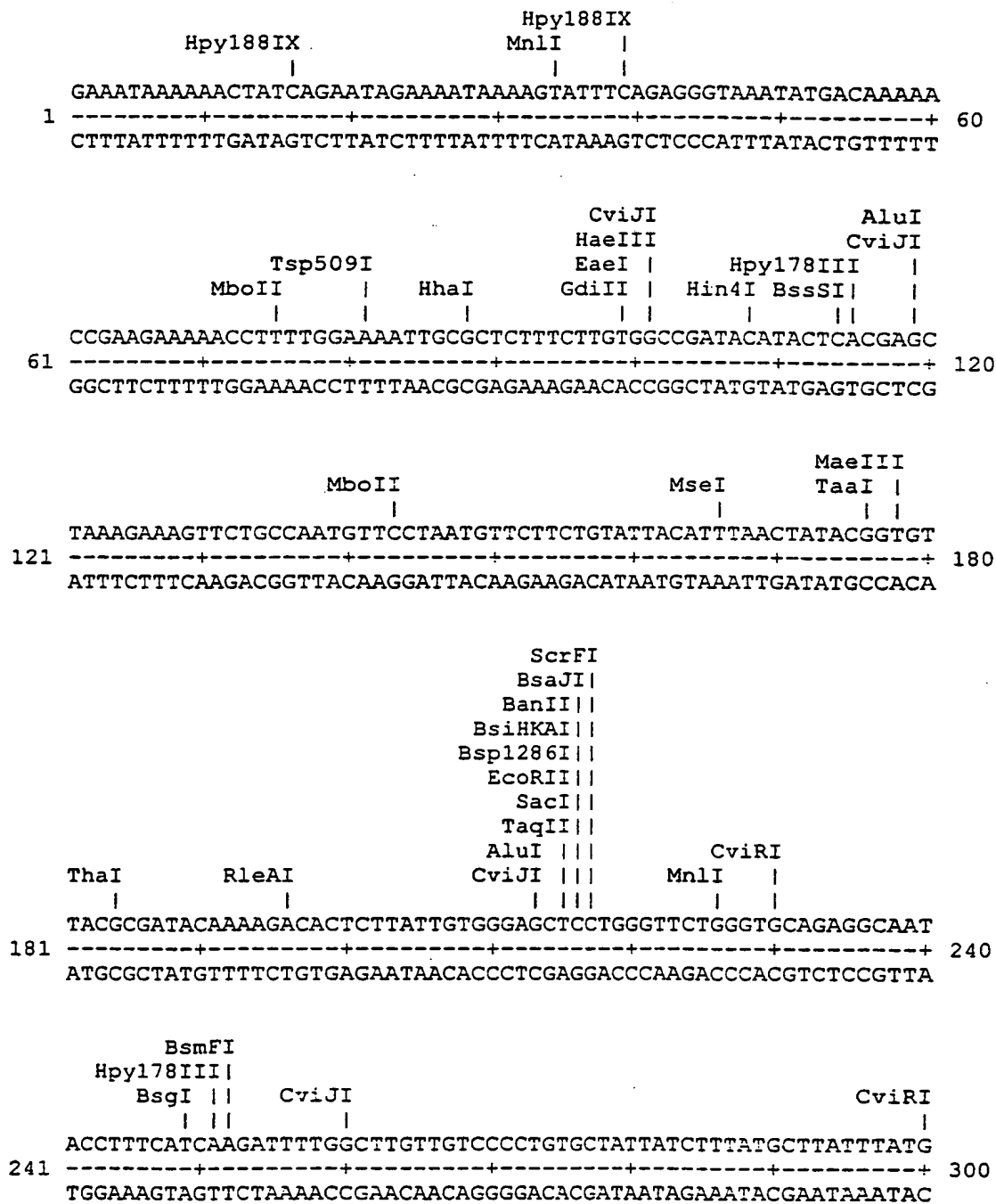
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Figure 2: Restriction enzyme analysis of the *C. pneumoniae* ATP/ADP translocase gene.



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Figure 2 (continued)

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                                CviJI
                                HaeI
                                HaeIII
                                StuI
DdeI      MseI      BtsI
AluI|      SspI|      CviRI|TspRI      MseI
CviJI|      |      |      |      |
||      |      |      |      |
CAAAGCTAAGTAATATTTTAAGTAAGCAGGCCTTATTTTATGCAGTGGGAACGCCCTTTT
301 -----+-----+-----+-----+-----+ 360
GTTTCGATTCATTATAAAATTCATTTCGTCCGGAATAAAATACGTCACCCCTGCGGGAAAA

                                Tsp509I      ThaI
                                Sth132I|      FokI|
Tsp509I      Hpy178III TaaI|      |      |      SfcI
|      |      |      |      |      |      |
TAATTTTCTTTGCCCTGTTCCCGACTGTAATTTATCCGCTACGCGATGTTTTACATCCTA
361 -----+-----+-----+-----+-----+ 420
ATTAAAGAAACGGGACAAGGGCTGACATTAAATAGGCGATGCGCTACAAAATGTAGGAT

                                BccI
                                CviJI|
                                HaeI|
                                HaeIII|
                                BslI|      |
                                BpmI|      |
                                CjePI|      |
ApoI      TaaI|      |      |      |      |      |      |
Tsp509I      FokI|      |      |      |      |      |      |
|      |      |      |      |      |      |      |
CAGAATTTGCTGACCGTTTACAGGCCATCCTACCTCCAGGATTGCTAGGACTCGTTGCCA
421 -----+-----+-----+-----+-----+ 480
GTCTTAAACGACTGGCAAATGTCCGGTAGGATGGAGGTCCTAACGATCCTGAGCAACGGT

                                MseI      BsrI      CviRI
AflIII|      BspGI|      Fnu4HI|      RsaI
SmlI|      BbvI|      |      |      |      |      |
||      |      |      |      |      |      |
TCTTAAGAACTGGACATTTGCTGCATTTTATGTAAGTGAAGTATGGGGAAGCGTCA
481 -----+-----+-----+-----+-----+ 540
AGAATTCTTTGACCTGTAAACGACGTAAAATACATGAACGACTTGATACCCCTTCGCAGT

                                NlaIII      Tsp509I
                                |      |
TGCTATCTCTAATGTTCTGGGGATTGCTAATGAAATTACAAAAATCCACGAAGCAAAGC
541 -----+-----+-----+-----+-----+ 600
ACGATAGAGATTACAAGACCCCTAAACGATTACTTTAATGTTTTTAGGTGCTTCGTTTCG

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Figure 2 (continued)

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                                MunI
                                Tsp509I
                                Tth111II
                                AluI
                                CviJI
                                Hpy188IX | SspI
                                BfaI |
                                CviRI
GTTTCTACGCTCTTTTCGGTATCGGAGCTAATATTTCTTTACTAGCTTCTGGTCGTGCAA
601 -----+-----+-----+-----+-----+-----+-----+ 660
CAAAGATGCGAGAAAAGCCATAGCCTCGATTATAAAGAAATGATCGAAGACCAGCACGTT

                                BsaJI
                                StyI
                                DpnI
                                BstYI | | ApoI
                                Sau3AI | | Eco57I
                                AluI
                                CviJI Hpy188IX AlwI | | Tsp509I
                                CviJI
TTGTTTGGGCTTCAAAGTTGAGAGCTTCCGTTTCTGAAGGTGTAGATCCTTGGGGAATTT
661 -----+-----+-----+-----+-----+-----+ 720
AACAAACCCGAAGTTTCAACTCTCGAAGGCAAAGACTTCCACATCTAGGAACCCCTTAAA

                                AlwNI
                                BslI
                                PflMI
                                MaeIII |
                                BsrI | |
                                CviJI | |
                                HaeI | |
                                HaeIII | |
                                MscI | |
                                CviJI
                                BccI |
                                BspGI
                                EaeI | | |
MaeII BaeI | | Hpy178III | BaeI | | |
| | | | |
CTTTACGTCTTTTGATGGCTATGACTATTGTATCTGGACTTGTTCTTATGGCCAGTTACT
721 -----+-----+-----+-----+-----+-----+ 780
GAAATGCAGAAACTACCGATACTGATAACATAGACCTGAACAAGAATACCGGTCAATGA

                                DpnI
                                DpnI
                                Hpy178III
                                Sau3AI |
                                MnlI |
                                MboII
                                BsrI | | AlwI | AlwI | |
                                TaqII | | CviRI |
                                | | | |
GGTGGATCAATAAGAACGTATTGACCGATCCTCGCTTCTATAATCCAGAAGAAATGCAAA
781 -----+-----+-----+-----+-----+-----+ 840
CCACCTAGTTATTCTTGCATAACTGGCTAGGAGCGAAGATATTAGGTCTTCTTTACGTTT

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Figure 2 (continued)

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                                                    BglII
                                                    BstYI
                                                    Sau3AI
                                                    AluI
                                                    CviJI
                                                    BfaI
                                                    MnlI
                                                    |||
AGGGGAAAAAAGGTGCTAAACCTAAATGAATATGAAAGATAGCTTCCTCTATCTTGCTA
841 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 900
TCCCCTTTTTTTCCACGATTTGGATTTTACTTATACTTTCTATCGAAGGAGATAGAACGAT

                                                    MseI
                                                    CjePI
                                                    MseI
                                                    CviRI
DpnI
AluI
CviJI
GATCTCCTTATATTCTTTTATTAGCTCTCTTGGTTATTGCCTATGGTATTTGCATTAAC
901 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 960
CTAGAGGAATATAAGAAAATAATCGAGAGAACCAATAACGATAACCATAAACGTAATTGA

                                                    CviRI
                                                    MwoI
                                                    CjePI
AluI
CviJI
MaeIII
Tsp45I
TaqI
MspAII
PvuII
SfcI
TAATCGAAGTGACTTGGAAGTCAGCTGAACTGCAATATCCTAATATGAATGACTATA
961 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1020
ATTAGCTTCACTGAACCTTTTCAGTCGACTTTGACGTTATAGGATTATACTTACTGATAT

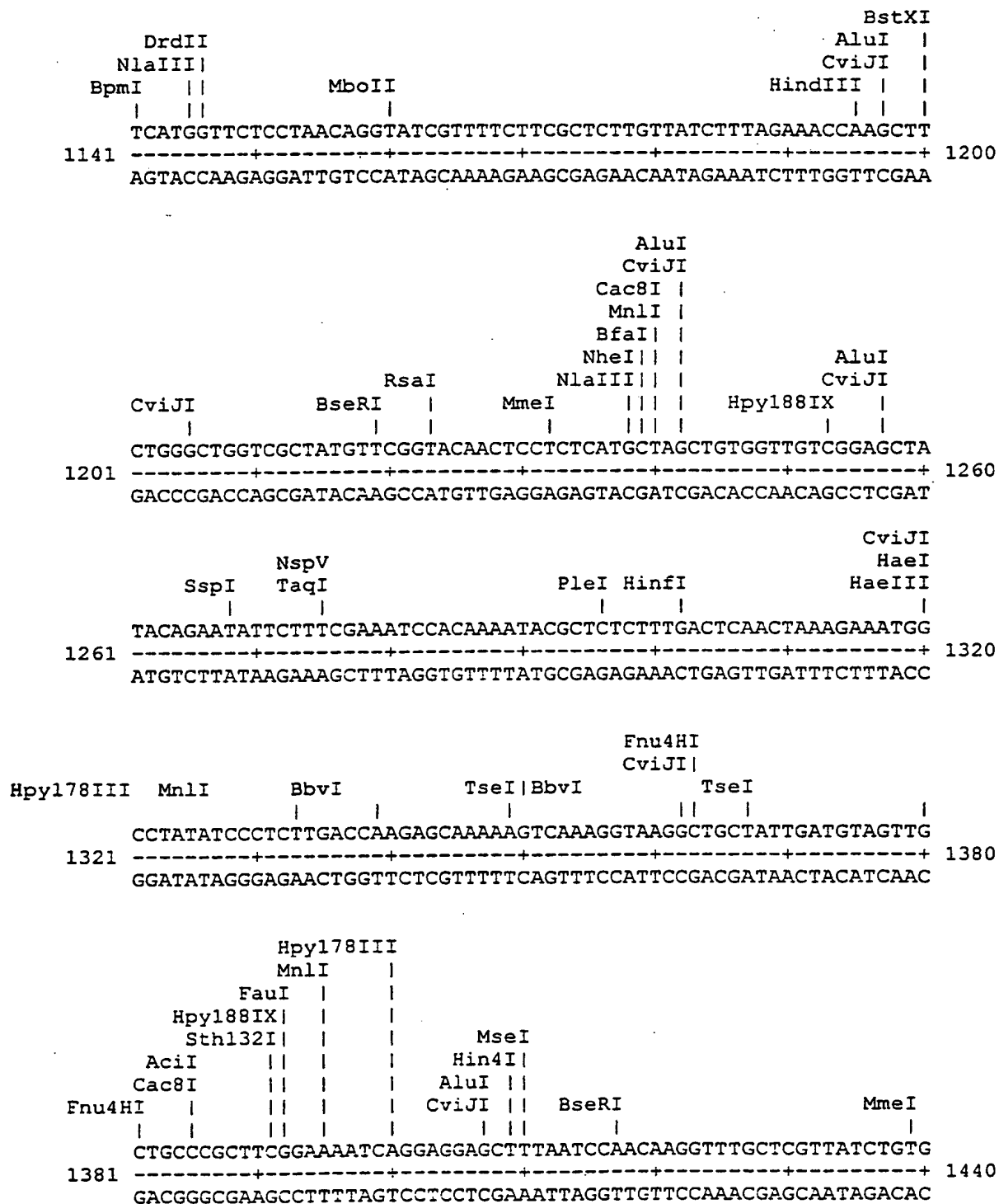
                                                    BspGI
                                                    BciVI
NlaIII
Hpy178III
BsrI
RsaI
NlaIII
GTGAGTTCATGGGGAACCTTCTCCTTCTGGACTGGCGTAGTATCCGTACTTATCATGCTAT
1021 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1080
CACTCAAGTACCCCTTGAAGAGGAAGACCTGACCGCATCATAGGCATGAATAGTACGATA

                                                    MaeIII
                                                    Tsp45I
                                                    BfaI
                                                    BanII
                                                    BsaXI
                                                    Bsp1286I
                                                    Hin4I
                                                    HincII
                                                    CviJI
                                                    HpaI
                                                    BsrI
                                                    MseI
                                                    NlaIV
                                                    FokI
MaeII
MaeIII
Tsp509I
BccI
TTGTTGGTGGTAACGTCATTCGTAAATTGGGATGGTTAACTGGAGCCCTAGTCACTCCTG
1081 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1140
AACAACCACCATTGCAGTAAGCATTTAACCTACCAATTGACCTCGGGATCAGTGAGGAC

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Figure 2 (continued)



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Figure 2 (continued)

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                                TspRI
                                HinfI |
                                TfiI |
                                SimI
                                AluI | HaeIV
                                CviJI | Hin4I
                                BtsI | |
                                CviRI | |
                                MboII | |
                                BsrDI
                                |
1441 GAAGTATTGGAGCTATGACCCCTTATCTTGCA GTGATTCTTCTTTTCATCATTGCTATTT
-----+-----+-----+-----+-----+-----+-----+-----+ 1500
CTTCATAACCTCGATACTGGGGAATAGAACGTCAC TAAGAAGAAAAGTAGTAACGATAAA

                                Bce83I
                                DdeI
                                CviRI | MseI
                                DdeI HhaI | CjeI | |
                                MwoI MseI |
                                | | | |
1501 GGTTGGTTTCTGCAACTAAGTTAAACAACTATTCTTAGCGCAGTCTGCTCTTAAAGAAC
-----+-----+-----+-----+-----+-----+-----+ 1560
CCAACCAAAGACGTTGATTCAATTTGTTTGATAAGAATCGCGTCAGACGAGAATTTCTTG

                                AlwNI
                                MboII
                                MboII |
                                Hpy178III AluI | |
                                SmlI | HinfI CviJI | |
                                CviJI | | TfiI CjeI | | | AceIII
                                | | | | | | |
1561 AAGAAGTGGCTCAAGAAGATTTCAGCTCCTGCTTCTTCATAGAGTTGCTTCTTACTCTT
-----+-----+-----+-----+-----+-----+-----+ 1620
TTCTTCACCGAGTTCTTCTAAGTCGAGGACGAAGAAGTATCTCAACGAAGAGAATGAGAA

                                DpnI
                                Sau3AI |
                                | |
                                BspMI
                                |
1621 GTTGATCCCTACCTGCTTTT
-----+-----+-----+ 1640
CAACTAGGGATGGACGAAAA

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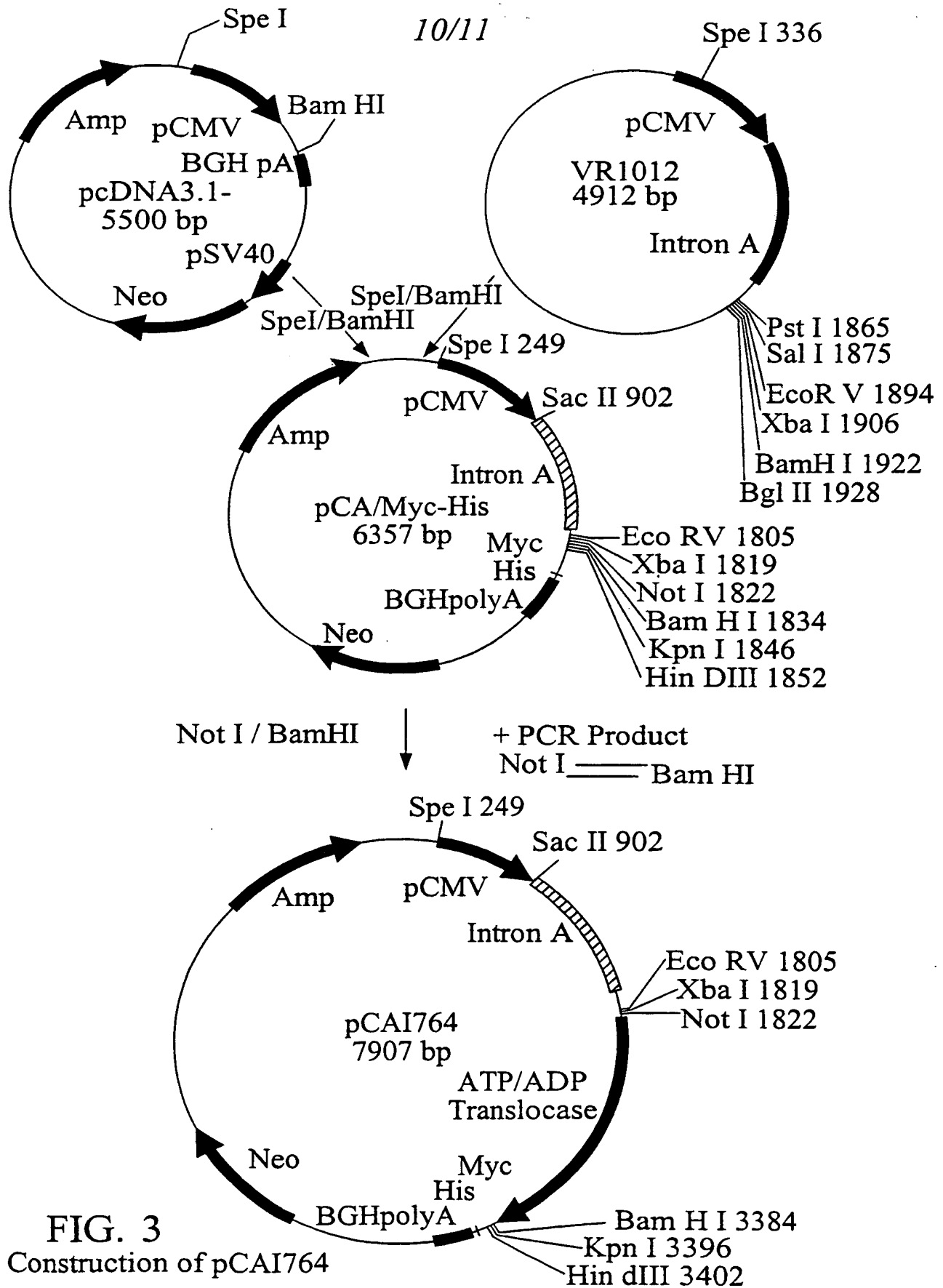


FIG. 3
Construction of pCAI764

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Figure 4: Protective Efficacy of DNA Immunization with pCAI764

